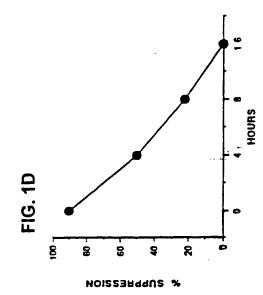
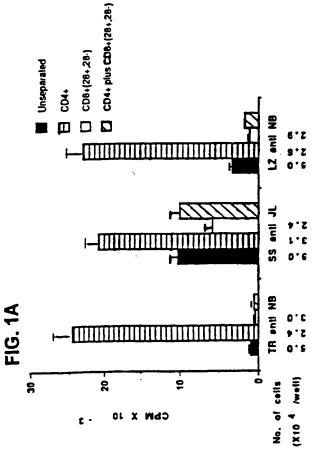
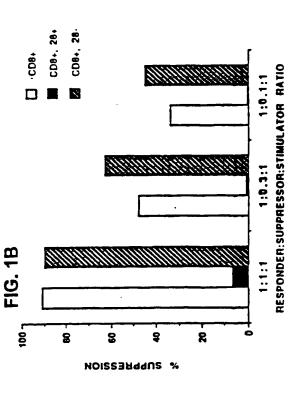


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TCL SS anti-JL

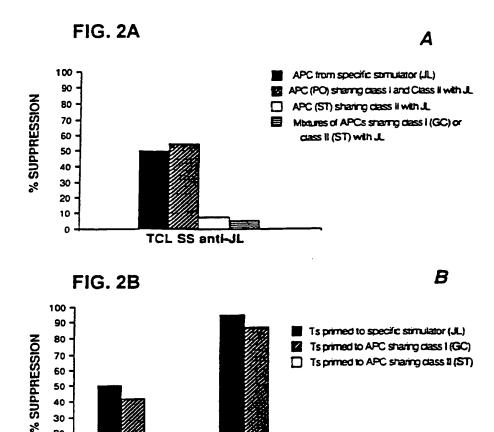
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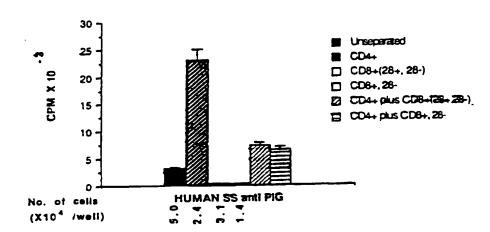
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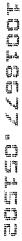


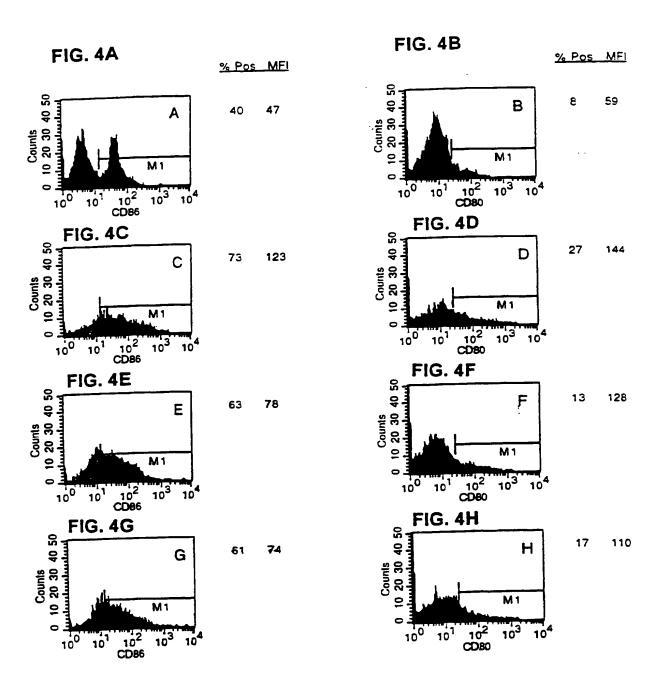


º MLC SS anti-JL

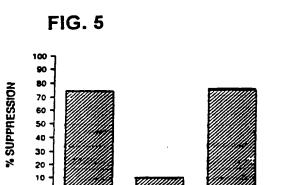
FIG. 3







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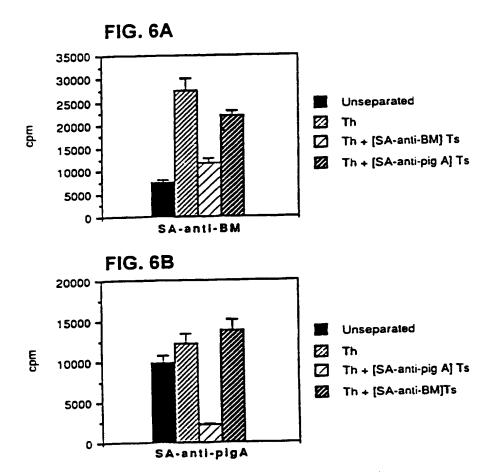


enti-CD28

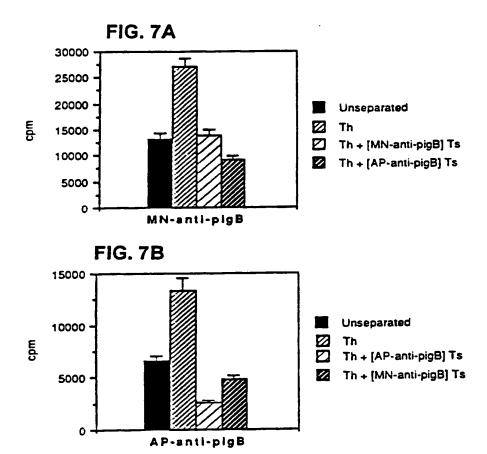
enti-CTLA-4

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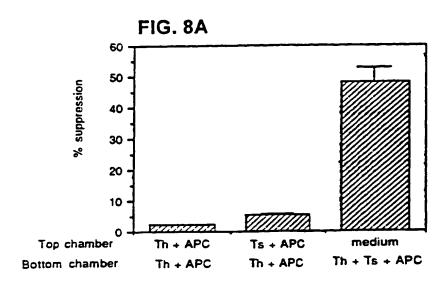


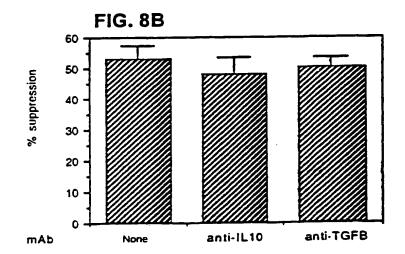




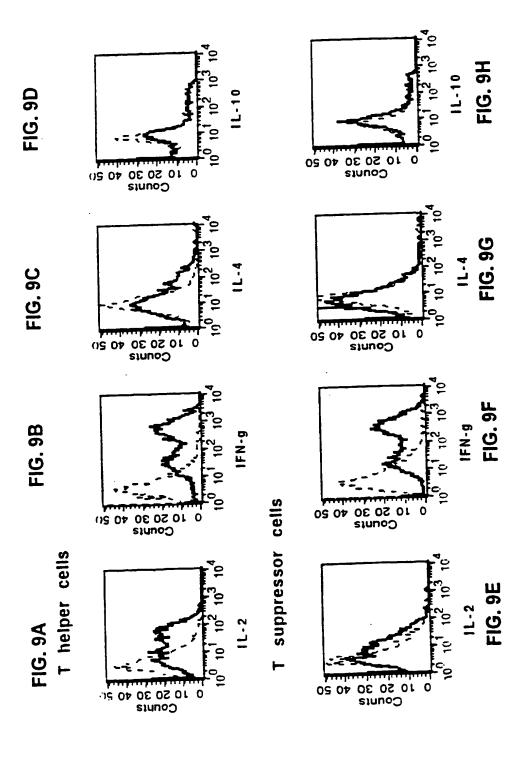


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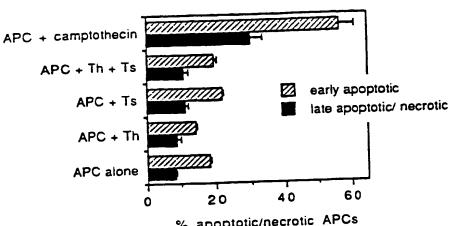


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% apoptotic/necrotic APCs

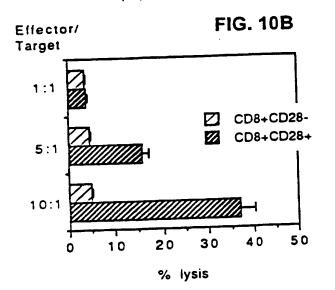
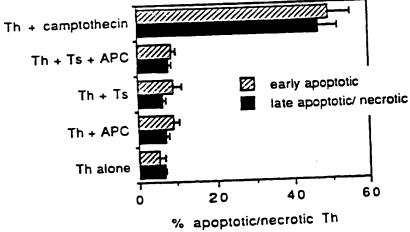
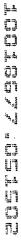
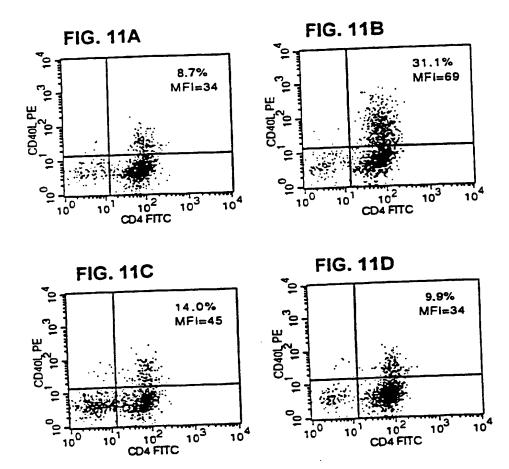
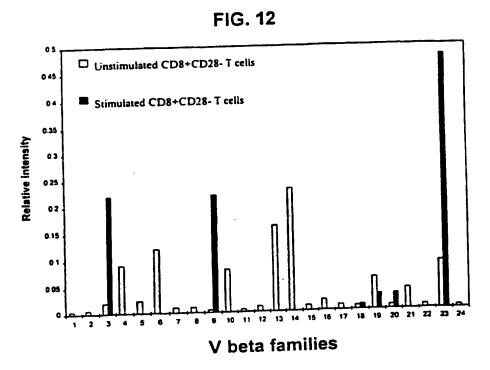


FIG. 10C

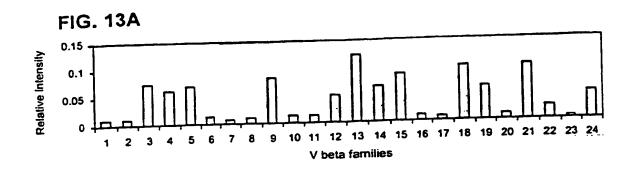


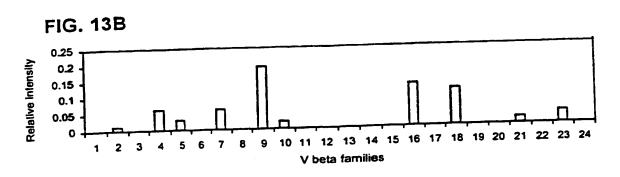


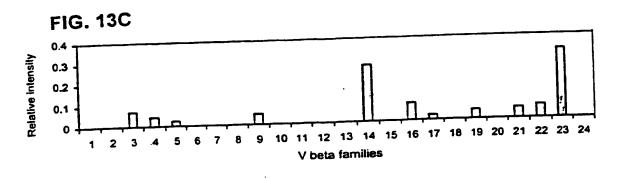




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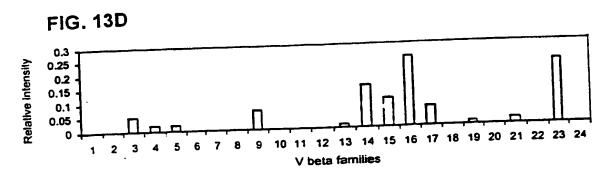
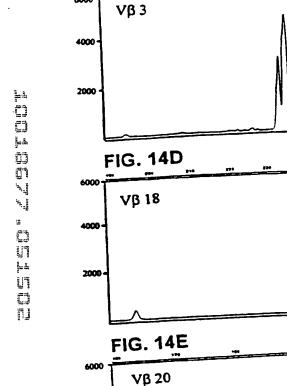


FIG. 14A

6000

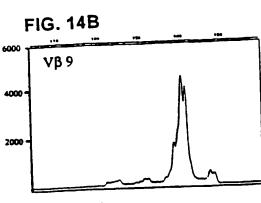
14/44

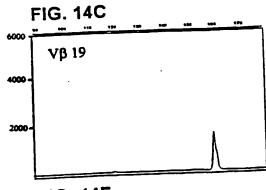


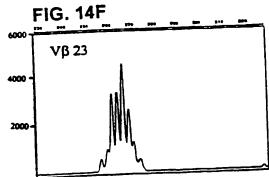


4000

2000







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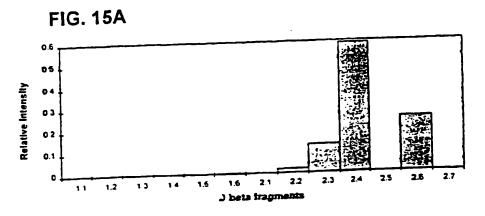


FIG. 15B

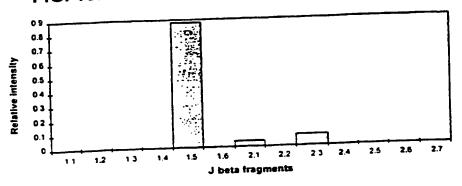
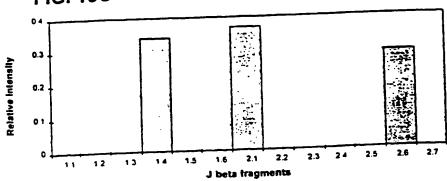


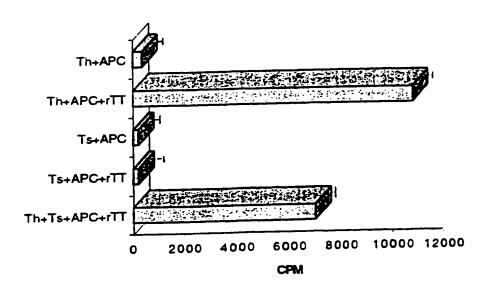
FIG. 15C



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FIG. 16





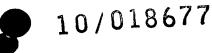
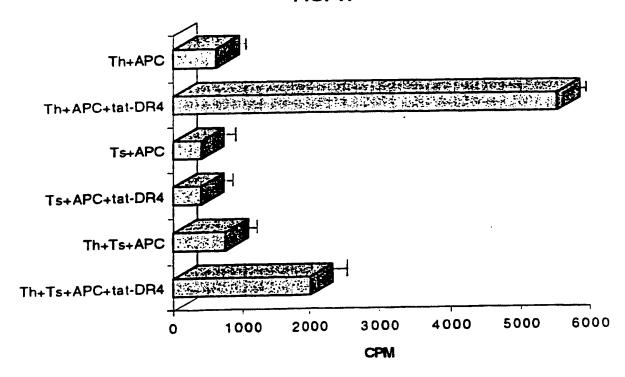


FIG. 17



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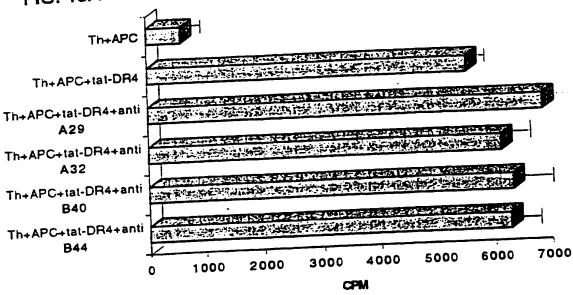
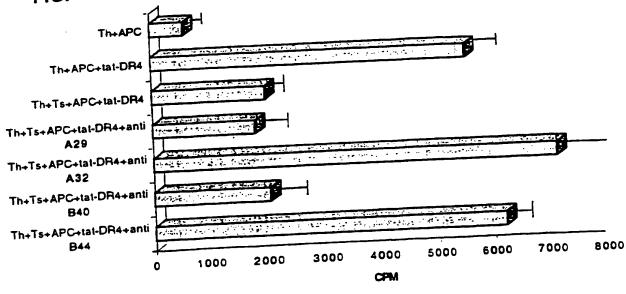


FIG. 18B



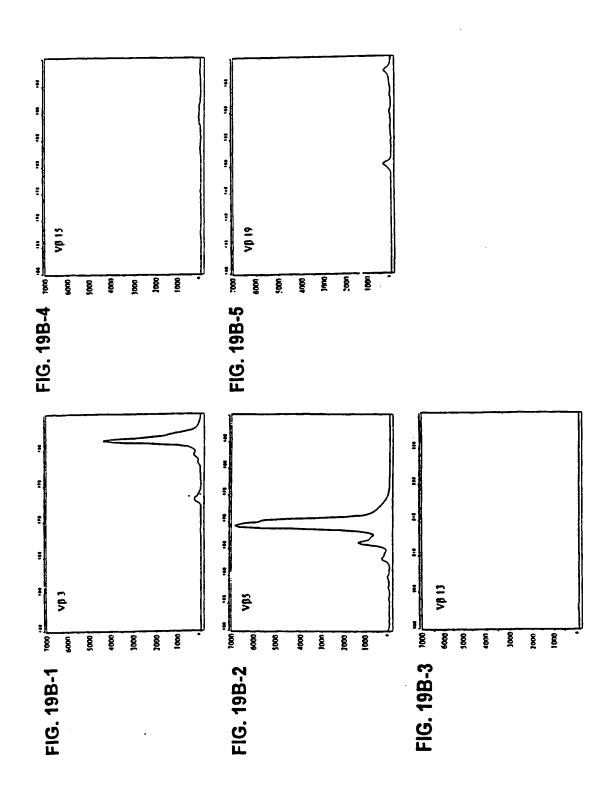
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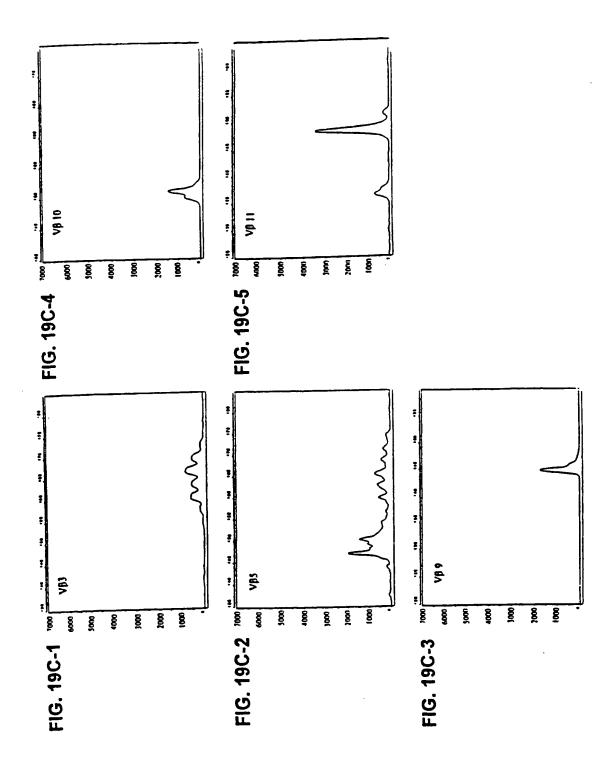


VB 15 FIG. 19A-5 700 F FIG. 19A-4 100 3000 3000 **VB3** FIG. 19A-2 " 200 FIG. 19A-3 FIG. 19A-1

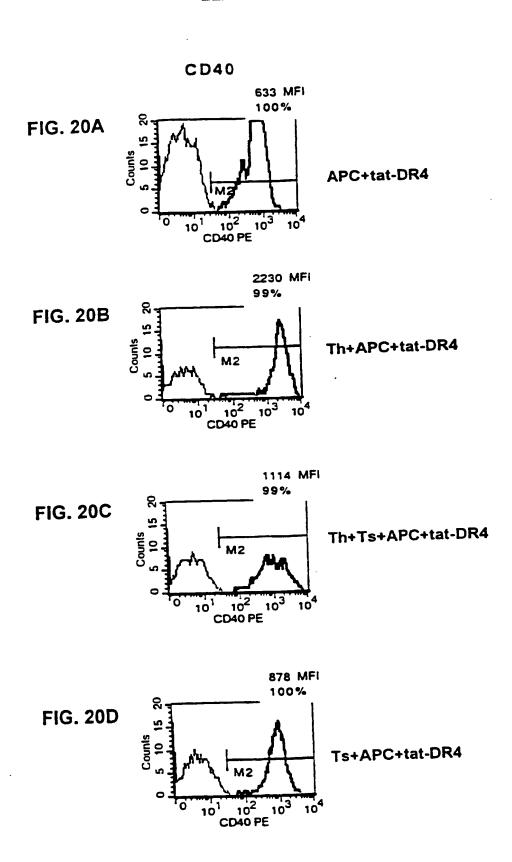




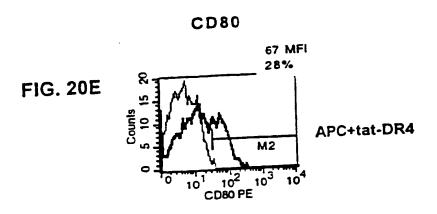
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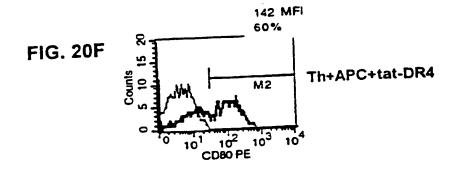


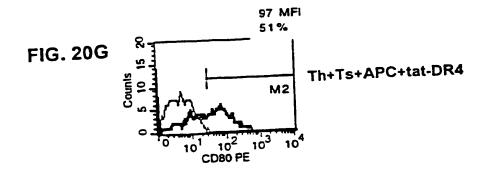
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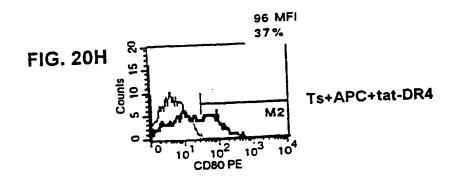


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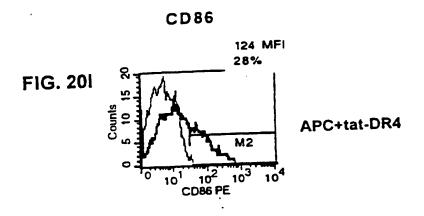


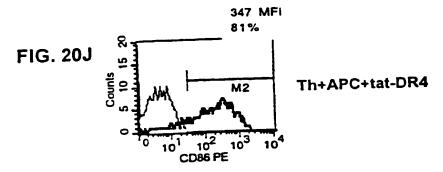


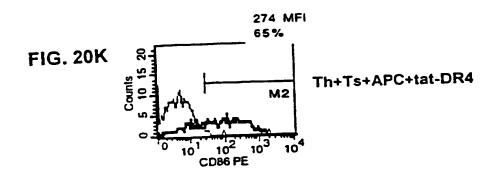


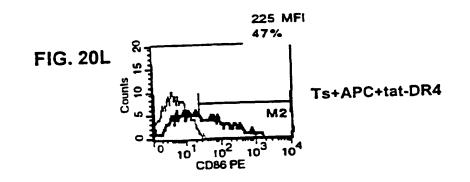
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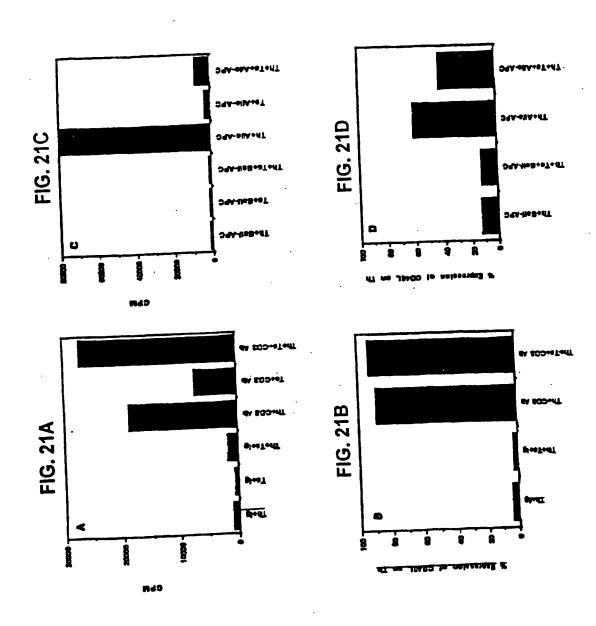




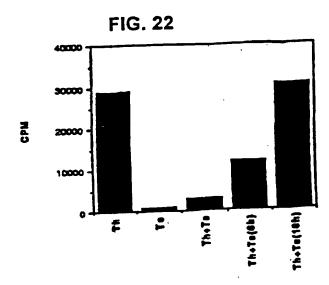




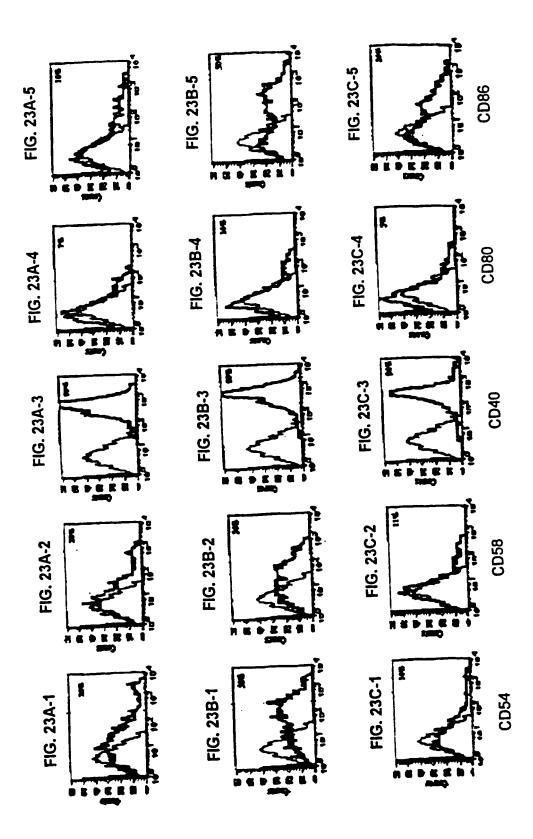




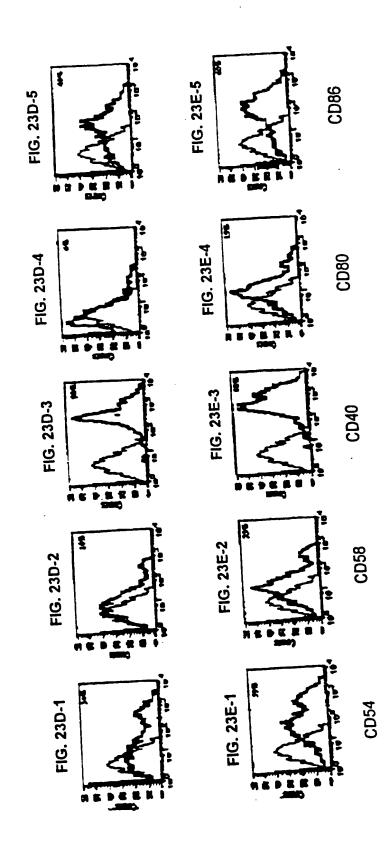
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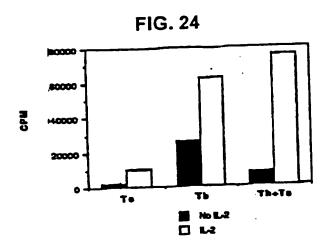


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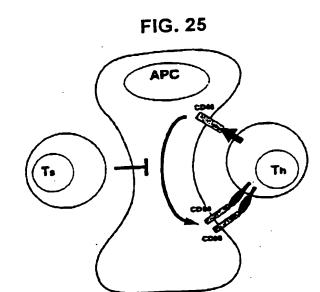
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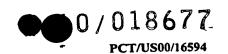


FIG. 26

HLA A, B and DR Antigen Values and Split Equivalences

	HLA A, B and	DR Antigen ve		DP.	
A		_B:	FOUIVALENT	FOCUS	EQUIVALENT
A 1.0CUS 1 2 3 3 10 11 19 23 24 25 25 25 25 29 30 31 32 33 43 66 68 69 74 80 • 203 • 2403 • 99	1 2 3 9 10,66 11 19,74 22 24 25 28 21,61,59 29 30 31 32 33 34 38 43 68,10 68,23 74,19 80 203 210 2403 99	TOCUS 5 7 8 12 13 14 15 16 17 22 27 35 37 38 39 40 41 42 44 44 44 45 48 49 60 61 62 63	EQUIVALENT	DR EOCUS 1 2 3 4 6 6 7 8 8 10 11 12 13 14 15 16 17 18 61 62 63 - 1803 - 1404 99	EQUIVALENT 1 2.15.16 3.17.18 4 5.11.12 6.13.14 7 8 9 10 11.5 12.5 13.5 14.6 18.2 17.3 18.3 81 82 81 82 81 82 81 82 81 82 81 82 81 82 83 1403 1404 89
		54 55 58 59 60 61 62 63 64 65 67 70 71 72 73 75 76 77 • 703 • 3901 • 3902 • 4005 • 5102 • 5103 • 7801 • 8101 • 99	55.22 56.22 57 58.17 59 60 61.40 62 63 64.14 65.14 67 70.71.72 71.70 73 75.15 76.15 77.15 703 3901 3902 4005 5103 7801 8101 99		

Code 99 means not tested

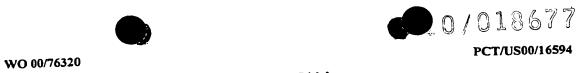




FIG. 27A

DRB Protein Sequences - 20th March 1998 - SGE Marsh ANRI

1	10	20	. 30	40 .	50	60	70	80	90	100		
RB1*0101	•	•			,	NIOSE	ርኒ/Dፑፐ	SDVGF	YRAV	TELGRPD	AEYW!	1SQK
DTRPRFL'	WQLK	FECH	FFNGTI	RVRL	LERCI	YNUEE	77 2 1 1 1 1	,5D V G2				
LLEQRRA	AVDT	YCRH	NYGV	jest i v	VQKKV					AV		
RB1*0102												
RB1*01022	****	• • •										
V******								ll	DE	V		
RB1*0103									N·	V	V	_
KB1-010+	1	P-	R	F-D	-YF		-F		!A		V	
KB1-1201	. ——	•					_		1	Α	V	
RB1*1501	2 ***	**	P-R	F-	D-YF-				1		·	
*******	_						t -		IA	, 		-Q-
RB1+1502	1	P.	.R	F-D	-YF					•		
					- D VI	E	F		[—A		
RB1*1502	2 ***	****	*****		·r-W- 11		•					
RB1*1502	*****	•	D D	F	D-YF-		F		I-	-A		
RB1*1502	.3	* *	-P-K		-D-11						••	_
******	*****	• D.	D	F-D	-HF		-F		IA		. V	\ <u>\</u> -
			1			•			_	-A	V	_
*** ORB1*1504	***	***	-P-R	F	-D-YF-		F			_A	y	
)KB1_100	, ;*						_			_A	V	
ORB1*1505	5 ***	***	-P-R	F	-D-YF-		r			-A		
******				_			F_	-A		IA	V-	
DRB1*150	5 ***	****	_P-R		F-D-Yr							
******	*****		_	E 1) VF				F-I)		Q-
DRB1*160	11 —	F	7-R	[-1	<i>J</i> -11)		
DRB1*160			D.D	F	-D-YF				F-	-D		•
DRB1*160	12 **	~ ~ ~	-r-K	-					_			
*********			P.R	F-l	D-YF-				L	-D		~~
DKR1-100	21 ++	****_	P-R		F-D-YF	·				-D		
DKD1, 100	*****	**						_	F_T)-A		Q
DDB1+160	3	F	-R	F-I)-YF)-A		_
									I	-DL		
- DRB1*160)4 **	****	•P-R		-F-D-Y							
									I	D		
DRB1*166)5 **	****	P-R-		r-D- 1 1							
******		*	_P-R						I	-D		
DRB1*16	• •	***	-P-R		. ED-11							
******			P-R	1	F-D-YF	N-				F-D		
DRB1*16	08 **	¥ * *									N	17-
******		-	VCTC		Y-D-Y	FHN	1	-F		K-GR	N	V -
DRB1*03	011 -		.1313-							К-С	:D_N_	
_H			TVCTC	·	Y•D	YFH	-N	F			31/14	

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•	FIG. 27B	
	YFHN	K-GR-N
DRB1*03021 ——EYSTS——F		OD N
H—— DRB1*03022 ——EYSTS——F	-YFH-N-	K-GRN
DRB1*03022 ——EYSTS——F		K-GRNV
DRB1*0303 *******YSTS	FYFHN	K-OK-IV
_*******	_Y-D-YFH	FK-GR-NV-
DRB1*0304 ******-EYSTS	_Y-D-Yrn	
********	-Y-D-YFHN	—FK-GR-N
DRB1*0305	-1-0-1111	
_******** DBB1*0306 ******-EYSTS	_Y-D-YFHN	K-GR-NV
DKD1 0300		F
DRB1*0307 ——EYSTS——F	D-YFH-N-	-F
-H	Y-D-YFHN	_FEK-GR-NV
13K B 1*U3V0		
-H	Y-D-YFH-RN	FK-GR-N
DRR1*0310EYSTS	Y-D-YFHN	_FA_HK-GR_NV
DRBI+0310		
DRB1*0311 *****—EYSTS——	_Y-D-YFHN	FK-GQ-NV
+++++++	F-D-YF-HY	Y-
DRB1*04011E-V-H	-D-11-11-1	
E DRB1*04012 *****-E-V-H	_F-D-YF-HY	K
2.2.	1	
DRB1*0402E-V-HF	-D-YF-H-Y-	
*****	- D.VE.U. V	VY-
DRB1*0403 ——E-V-H	-D-YF-HY	••
E	F-D-YF-H-Y-	VY-
DRB1*0404		
E DRB1*04051E-V-H	F-D-YF-HY	SS
DRB1*04052 ******-E-V-H	F-D-YF-HY	
*****	F-D-YF-H	
2. —		.
E DRB1*0407E-V-H	F-D-YF-H-Y	E
DRB1*0408 *****-E-V-H	F-D-YF-HY-	
	F-D-YF-HY	SKK
DKR1-0-103		17
DRB1*0410 ******-E-V-H	F-D-YF-HY	S
D.C.		- VY-
DRB1*0411 ——E-V-H——	-F-D-YF-HY	SE
2.01		SI-DLV
E DRB1*0412 ******-E-V-H	F-D-YF-HY	
**************************************	F_D_YF-HY-	VV
DIADI VIII		
DRR1*0414 *********************************	F-D-YF-HY	IDE
DRB1*0414		



			FIG.	210				
DRB1*0415	*****_	-E-V-H	F-D-YF-I	HY		E	FD	V-
DRB1*0416	****	*****	F-D-YF-	н		Q	К	
DRB1*0417	****	*****	F-D-YF-	-HY		S	E	
DRB1*0418	****	*****	F-D-YF-	-н			IDL	V
DRB1*0419	******	••••*H	F-D-YF	-H				
DRB1*0420	*****	******	F-D-YF-	-Н			E	.cara
********	****						К	·
DRB1*0421	*****	**E-V-H						V
DRB1*0422	******	••E-V-H					~	
DRB1*0423	*****_	-E-V-H	F-D-YF-					V-R
DRB1*0424	*****_	-E-V-H	F-D-YF-			S		17
DRB1*0425	*****	*-E-V-H	F-D-YF	-HY		 	FDL	V-
DRB1*0426	*****_	-E-V-H	F-D-YF-	HY		T		
DRB1*0427	*****_	-E-V-H	F-D-YF-	н	,		E	AV
*****	,	EVETE	F-D-YF	Y	F	—Е	-F-D	
DRB1*11011		EYSTS	F-D-YF-		F	E	_F_D	
DRB1*11012 H—-*			-	FY	F	E	F-D	
DRB1*11013		EYSTS				_	. 55	17
DRB1*1102		EYSTS	F-D-YF			_	-IDE	V
H DRB1*1103]	EYSTS	F-D-YF	Y	F	E		V
H—— DRB1*11041		EYSTS	F-D-YF-					V
DRB1*11042								V
H DRB1*1105		-EYSTG						
DRB1*1106							FD	
DRB1*1107	*****	**-EYSTS	F-D-Y	FY-	F-	Е	K-GR-	-NV
DRB1*1108	*****	******S	F-D-Y	FY-	F	——Е	D	
DRB1*11082		******S	F-D-Y	FY-	F	—Е-	D	
DRB1*1109	•	**,*******						
*******		******						
DRB1*1110	*****							

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35/44 FIG. 27D

		FIG. 21 D				
DRB1*1111	******** <u>S</u>	F-D-YFY	F	—Е	FDE	
*********	•		_	E	-F-D	
DRB1*1112	*********	—-F-D-YFF	[-c		
****	EYSTS——	-F-D-YFHF	-F	-E	R	V
DRB1*1113	E1313					
DRB1*1114	EYSTS	_F-D-YFY	F	·E	-IDE	
******		_F-D-YFDL	E	_F	_FD	
DRB1*1115	EYSTS					
H	*****-EYSTS	F-D-YFHN	F	—Е	IDE	V
DRB1*1116						_V
DRB1*1117	EYSTS-	_F-D-YFH—F		-E	RE	
H		F-D-YFY	F	—Е	I-D	V
DRB1*1118	*****-EYSTS					
**************************************	*****-EYSTS	F-D-YFY	F	E	I-D	
DRB1*1119						·····
DRB1*1120	******-EYSTS	F-D-YFH—N—	 	C		
******		F-D-YFY	F	—Е—	I-DE	AV-
DRB1*1121	******-EYSTS					
DRB1*1122	****-E-V-H	F-D-YFY	F	—Е	FD	
********	****	F-D-YFY	E	F	F-DL	
DRB1*1123	****-EYSTS					
*********	******-EYSTS	F-D-YFD	F	E	F-D	
DRB1*1124						V
DRB1*1125	*****-EYSTS	F-D-YFY	F	E		·
******		F-D-YFY	F	E		
DRB1*1126	*******-EYSTS	_				
DRB1*1127	*****-EYSTS	F-D-YFY	F	E	FDN-	
********	****	m N	F	F	FD	
DRB1*1128	****-EYSTS	F-D-YFN		<u>_</u>		
******	*****-EYSTS	F-D-YF	F	E	F-D	
DRB1*1129				_	- D	
DRB1*1130	****-EL-S	F-D-YFY	F		r <u>U</u>	

DRB1*1131	EYSTS		•		_	
H	EYSTG-Y-	HFHLL	F	VS-	I-D	AV
DKB1-1201			-	v	CF_D	
DRB1*1202	el *****—EYSTG-Y	HFHLL-	r-	V -	-01	
AV*****	******** 2 ******-EYSTG-Y	HFH-LL	F-	V	-SF-D	AV-
DRB1*1202	2 ******-EYSTG-Y	11111	-			17
DRB1*1203	2 *****-EYSTG-Y	HFHLL-	F	V-	-SID	V
*********			t		:I_D	
DRR1+120-	+ *******EYSTG-	HFHLL		[
AV*****		HFHFL-	F	V-	-SID	AV
DRB1*120		111.1.				
_++++++	•					



36/44 FIG. 27E

		FIG. 27E			
DRB1*1301	EYSTS	F-D-YFHN	F	I-DE	V
H DRB1*1302	——EYSTS——	F-D-YFHN	F	IDE	
H DRB1*13031	EYSTS	F-D-YFY	S	IDK	
H* DRB1*13032	******-EYSTS	F-D-YFY	S-	IDK	
DRB1*1304	EYSTS	F-D-YFY	_FS	I-DE	V
H* DRB1*1305	****-EYSTS-	F-D-YFHN	F	F-D	
DRB1*1306	******	F-D-YFHN	F	ID	V
DRB1*13071	******-EYSTS	F-D-YFY		FD	
DRB1*1308	*****-EYSTS	F-D-YFHF		IDE	V
DRB1*1309	*****-EYSTS	F-D-YFHN	F	IA	V
DRB1*1310	******-EYSTS	F-D-YFHN	F	I-DK	V-
DRB1*1311	******-EYSTS	F-D-YFY	F	F-D	V
DRB1*1312	****-EYSTS	F-D-YFY	S	ID	
DRB1*1313	*****-EYSTS	F-D-YFY	S	I-DL	
DRB1*1314	**********TS	F-D-YFY	F	F-D	3.7
DRB1*1315	*****-EYSTS	FYFHN	F	iDE	V
DRB1*1316	********EYSTS	F-D-YFHN-	F	IDE	
DRBI*1317	EYSTG-Y	F-D-YFY	F	I-DE	V
H DRB1*1318	*****-EYSTS	F-D-YFHN-		F-DL	H-
DRB1*1319	EYSTS-	FYFHF		IDE	•
DRB1*1320		F-D-YFHN			
DRB1*1321	——EYSTS——	F-D-YFY		I DE	V
DRB1*1322		F-D-YFY			
DRB1*1323	*****_EYSTS	F-D-YFY			V
DRB1*1324		F-D-YFY			——
DRB1*1325		F-D-YFY			
DRB1*1326		F—YFH—N—			



37/44 FIG. 27F

	•	FIG. 27F		- -
	*****_FV\$T\$	Y-D-YFHN	_FIDE	V
DRB1*1327				
DRB1*1328	******-EYSTS	F-D-YFHN	_}	
*******	**	F-D-YFHN	-FDE	
DRB1*1329	*****EYSTS			
DRB1*1330	*****-EYSTS	F-D-YFY	-FSI-D	
++++++++++	•		-FVIDE	
DRB1*1331	****-EYSTS	F-D-YFHN		
*******	****-EYSTS	F-D-YFHN	SIDE	V
DRB1*1332			SI-DKN	
DRB1*1333	*****EYSTS	F-D-YFY	_	
*******	##### TVCTC	F-D-YFHF	AHRE	V
DRB1*1401	EYSTS		_	
DRB1*1402	EYSTS	_F_YFH-N		
******		r veu N	DL	
DRB1*1403	EYSTS			V –
DRB1*1404	****-EYSTG-Y-	F-D-YFHF	A-HRE	V
DKB1.1404			RE	V
DRB1*1405	*****-EYSTSQ	F-D-YFH—F-		
_*******	*****-EYSTS	FYFHN		V
DRB1*1406			A_HR—E	
DRB1*1407	*******EYSTS	F-D-YFHF		
*******	***** ******-EYSTS	F-D-YFHF	HRE	V
DRB1*1408	*****-E1313			
DRB1*1409	*****-EYSTS	F-D-YFHN		
******		F-D-YFHF	A-HRE-	V
DRB1*1410		_	_ n 1	_
DRB1*1411	*******EYSTG-Y	F-D-YFHF-	ER	
A********	******	FYFHN	DL	
DRB1*1412	**********S	FYFHN		
V********		FYFHN		
DRB1*1413	*****	-	R-E-	
DRB1*1414	*****-EYSTS	F-D-YFH	RE	
*******	*	F-D-YFHF	F-DI	,V
DRB1*141) +++++++++++21O=1,	- -	4 U _I_DF_	V-
DRB1*1410	******-EYSTS	F-D-YFHF	A-H!DE-	,
********		F-D-YFHN		V
DRB1*141	7 *****EYSTS		- ·	V
*********	********EYSTS	FYFHN	R—E-	A
DRB1*141				
DRB1*141		—F—YFH—N——		
******	***	F—YFHF		V-
DRB1*142				
*******	•			



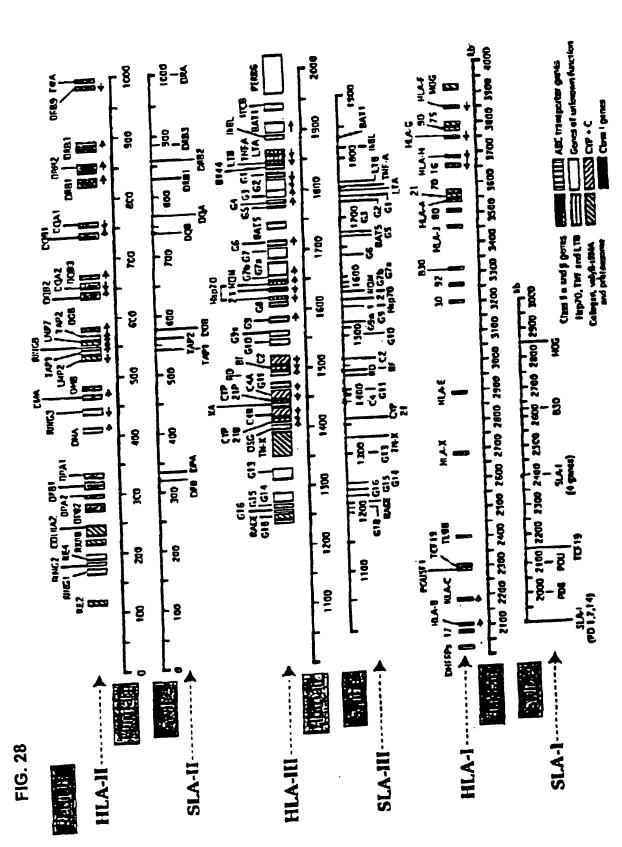
WO 00/76320 38/44

FIG. 27G

		FIG. 27G	
DRB1*1421	******-EYSTS	—F-D-YFH—N—	F
*********	***	F-D-YFHF	A-HF-D
DRB1*1422	*****-EYSTS		R-EV
DRB1*1423	*****-EYSTS	F-D-YFHF	
******** DRB1*1424	*****-EYSTS	FYFHN]—A————
H DRB1*1425	*******EYSTS	F-D-YFY	A-HF-D
******	***** *****—EYSTS	_QF-D-YFHF	
DRB1*1426		_	F-D-L
DRB1*1427	***** EYSTS	FYFHN F-D-YFHF	
DRB1*1428	*****-EYSTG-Y		AV
AV************ DRB1*1429	****-EYSTS	FYFHN	A
********* DRB1*1430	*****-EYSTS	F-D-YFHN	F
******	* *****-EYSTG-Y	F-D-YFHF-	
DRB1*1431	•		
DRB1*0701	_QG-YK	•	W
H-E DRB1*0703	*****G-YK	_QF_SLFF	V-SI-D-GQV
*******	EYSTG-Y	F-D-YFY	S——F–D—L
DRB1*0801		F-D-YFY	F-DL
DRB1*08021		-	F-D-L
DRB1*0802	2 *****-EYSTG-Y-	F-D-YFY-	
-H DRB1*0803	2EYSTG-Y-	F-D-YFY	SI-DL
H DRB1*0804		F-D-YFY	F-DLV
H*		F-D-YFY-	F-DLV
DRB1*0804			••
DRB1*0804		F-D-YFY-	
_******** DRB1*0805	****-EYSTG-Y-	F-D-YFY-	
DRB1*0806	****** PYCTC V.	F-D-YFY-	SF-DLV
********		F-D-YFY-	 -
DRB1*0807			
DRB1*080	*******EYSTG-Y-	F-D-YFY-	·
DRB1*080	· · · · · · · · · · · · · · · · · · ·	F-D-YFHF-	
******	******	F-D-YFY-	SI-D-LV
DRB1*081			
DRB1*081		F-D-YFY-	

FIG. 27H

	SI-D-LAV
DRB1*0812	*****-EYSTG-YF-D-YFY
	******-EYSTG-YF-D-YFY
DRB1*0813	*** SI_DL
DRB1*0814	*****-EYSRG-YF-D-YFY
*****	*****-EYSTG-YF-D-YFY
DRB1*0815	
DRB1*0816	*****—EYSTGYF-D-YFD
*****	*****
DRB1*0817	seess
DRB1*0818	*****-EYSTG-YF-D-YFY
******	*****-EYSTG-YF-D-YFYIDLI
DRB1*0819	V-SF-R-E-V
DRB1*09012	V U C
H-E	FFV——RVH—YA-Y——R——Q—
DRB1*1001	<u></u>



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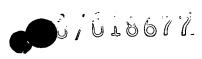
FIG. 29

	1				50
Sladra-0102					
Sladra-0202					
Sladra-0203					
Sladra-0101					
Sladra-02011					
Sladra-02012				TOTOMERDET	WEI FEECHE
Consensus	VENHVIIQAE	FYLSPDKSGE	EWE DE DODET	FHVDMEKRET	A MICTER GILL
					100
	51				
Sladra-0102					
Sladra-0202					
Sladra-0203					
Sladra-0101			-m		
Sladra-02011			-m		
Sladra-02012		TANDERNI F	TITERSNNTP	NTNVPPEVTV	LSDRPVELGE
Consensus	ASFEAQGALA	MIMADIME			
					150
	101				
Sladra-0102					
Sladra-0202					
Sladra-0203					
Sladra-0101		****			
Sladra-02011 Sladra-02012					
	PNILICETOK	FSPPVVNVTW	LRNGSPVTRG	VSETVFLPRE	DHLFRKFHYL
Consensus	thinger ross				
	151				200
Sladra-0102				-I	
Sladra-0202					
Sladra-0203					
Sladra-0101		,			
Sladra-02011					
Sladra-02012				YOUGH DEALE	MINICALC: IV
Consensus	PEMPSTEDVY	DCQVEHWGLD	KATTKHMELE	AQTPLPETTE	MIACYTOTIA
			228		
	201		220		
Sladra-0102					
Sladra-0202			h		
Sladra-0203					
Sladra-0101					
Sladra-02011					
Sladra-02012		LIIKGVRKGN	ATERRGPL		
Consensus	ALVGIIVGTV	TITIOANNA			

Group 01 has a leucine at residue 72 and Group 02 has a methionine. No other polymorphisms have been found in the alpha 1 domain.

Amino Acid Sequences of SLA DRA Alleles

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FIG. 30

	FIG. 50	5.0
	1 iaqffm g-sd-y fd-y	50
1	1 24 1	1 <u>r</u>
Sladrb-T	iaqffm g-sd-y fd-y	I-e-
Sladrb-N		
Sladrb-M		
Sladrb-Z		
Sladib-RD Sladib-C	iq-n cy-h-ry-hky l	f
		}
Sladrb-WX	iffm g-s	DSDVGEYRAV
Sladrb-Y	BOTTOBETHI LKFECHFFNG TERVELLERQ TIMEBELLERQ	
Consensus	RUIFFIII IIII	100
	81	
	51 64 k-v	
Sladrb-T		
Sladrb-N		
Sladrb-M		
Sladrb-Z		
sladrb-AD		
sladrb-C	id 9siqvs-s	
Sladrb-WX	id ssgys-s	
Sladrb-Y	HNYRILDTFL	VPRRAEPTVT
Consensus	TELGRPDAKY WNSQKDLLEQ RRAEVDTYCR HNYRILDTFL	
CONSCRE		150
	101	
Sladrb-T		
Sladib-N		
Sladib-M		
Sladrb-2		
Sladib-2		
Sladin-Au		
Sladrb-C Sladrb-WX		
Sladin-wv	S VYPAKTOPLO HENLLVCSVT GFYPGHVEVR WFRNGQEEA	GVVSTGLIPN
sladrb-Y	WYPAKTOPLO HENLLVCSVT GFYPGHVLVR WIRKOGE	-
Consensus	Altwiden	200
	151	
Sladrb-T		
Sladrb-N		
Sladrb-M		
Sladrb-Z	D	
Sladrb-A	D	
Sladrb-C		
Sladrb-W	X	MMXDOASTS
Sladrb-Y	ISPVIVEWE	W Varandores
Consensus	IS GOWTFOTMYM LEIVERS	
	237	
	201	
sladrb-T		
Sladib-N		
	Zv	
cladrb-2	Zv	
219012		
2190ID-V		
Sladrb-C		
SladID-W	V V	
Sladib-I	Y	
Consensu	ne and	

Amino Acid Sequence of SLA-DRB Alleles

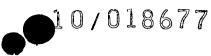


FIG. 31

		FIG. 37			
					50
	1			g	
-0021	·				
Sladga-02022					
Sladga-0101					
Sladga-0103			£	GDEEFYVDLE	
Sladga-0102		CVGVG	PSGYYTHEFD	GDEEFYVDLE	KKELAMOTER
Consensus	EDIAADHVAS	ACTMAIG219			
Consenses					100
	51 r				
1 02021					
Sladga-02021					
Sladga-02022					
Sladga-02023					
Sladga201					
Sladga-0101					
Sladga-0103		1-	A£	NNTAAVNQVP	COMMEDICIV
Sladga-0102	e	CRIPNIATAK	HNLNILIKRS	NNTAAVNQVP	FAIATIME.
Consensus	FSKFTSFDPQ	CHTV4 THEFT.			150
	101				
Sladga-02021					
Sladga-02022					
Sladga-02023					
S14004-02025					
Sladga-0201					
Sladga-0101					
Sladga-0103	1	5		VTEGFSETSF	LSKNDHSFLK
Sladga-0102	ACCOUNTED TO	HVDNIFPPVI	NITWLKNGAS	415G: 0010-	
Consensus	MPGGANITIC				200
	151				
sladga-02021			. '		
91adga-02022					
Sladga-02023					
Sladga-0201					
Sladga-0101					
Sladga-0103					
512002-0102			e MCT DEPT.T.KI	WEPEIPAPMS	ELTETVVCAL
Sladqa-0102	TOYLTELESD	DDFYDCKVE	H WGLDAF DELL	•	
Consensus	1012000			232	
	201				
	201				
Sladga-0202					
c1adga-0202	2				
sladga-0202	3				
51adga-0201					
c1adga-0101					
Sladga-0103			- 1		
Sladga-0102			- PSGCPSRHC	G SL	
219509-010-	GLIVGLVGIV	A ACLAETION	T man		
Consensus			132) and Group	02 is 232
		ia idole	tion at 134	,	

Group 01 is 231 amino acids (deletion at 132) and Group 02 is 232 amino acids

Amino Acid Sequences of SLA-DQA Alleles

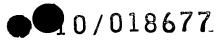


FIG. 32

					50
	1		_	63	
		ay-	ws-d-	fl-	my
Sladqb-D			ws-d-	fl-	
Sladqb-D2	I			fl- wv	
Sladqb-XA			1_	WV T	
Sladgb-2		y	i_t-	wvrya-	V
Sladgb-#			116-		nV
Sladqb-T			175_		
		a	b-t-	1-	
Sladgb-Y	F		g	1- YIYNOEEHVR	
Sladqb-C		OFFECTEN	GTORVR-VAR	YIYNQEEHVR	FDSDVGEFRA
Consensus	GRDSPQDFVY	Of ME Perry	33 5 31		
					100
	51				
Sladqb-D		-168			
Sladqb-D2		-1ea		2446	
			V		
Sladqb-XA					
Sladqb-Z		i	-t		
Sladqb-W					
Sladqb-T		_			
Sladgb-Y					
Sladqb-C		35	-WA-I	KHNYQIEEGT	TT OPPUOPTU
	WTPLCRPDAD	YWNGQKDVLE	OKRAELDIVC	YHMIÖTEEGI	TEGENAGET
Consensus	1112010 3	•			
	101				150
	101				
Sladqb-D					
Sladob-D2					
Sladgb-XA					
Sladgb-Z					
Sladgb-W					
Sladqb-T					
Sladqb-Y					
Sladqb-C		MURNT TUCAV	TDFYPSQVKV	OWFRNGQEET	AGVVSTPLIR
Consensus	TISFSKALAL	MINIMATINA	,		
					200
	151				
Sladqb-D					
Sladgb-D2				n	
Sladgb-XA					
Sladqb-Z					
Sladqb-W					
Sladqb-T					
Sladqb-Y				n	
Sladqb-C				TOSDITUENE	AOSESAOSKM
Consensus	NGDWTYOVLV	MLEMNLQRGD	AAACKAFFF	LOSPILVEWR	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
C0112 c112 GD					
	201		230		
	201	*======			
Sladob-D					
Sladqb-D2				•	
Sladqb-XA					
Sladqb-Z					
Sladqb-W					
Sladqb-?					
Sladqb-Y					
Sladqb-C			PHRSOKGLVR		
Consensus	LSGVGGFVLG	TELGLODE	RHRSQKGLVR		
= -					

Amino Acid Sequences of SLA-DQB Alleles